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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compugen
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                                                                                                                                                                            yene ox40 protein
laminin gamma-1 ch
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hypothetical prote	T23064	ν	2823	7.6	97	45
hypothetical prote	T34288	N	1827	7.7	97.5	44
furin (EC 3.4.21.7	S43656	N	837	7.7	97.5	3
trophozoite cystei	C42125	Ŋ	677	7.7	97.5	42
nerve growth facto	GQHUN	_	427	7.7	97.5	41
OX40 homolog - hum	137552	N	277	7.7	97.5	40
laminin alpha-1 ch	S14458	ν	3075	7.7	98	39
CD30 antigen precu	A42086	N	595	7.9	100	38
B-cell activation	A60771	N	277	7.9	100	37
laminin alpha-1 ch	MMMSA	H	3084	7.9	101	36
gene G4R protein -	D36858	N	349	8.0	101.5	35
G2R protein - vari	D72175	N	349	8.0	101.5	34
hypothetical prote	T28623	N	348	8.0	101.5	ω
M130 antigen precu	138004	N	1151	8.0	102	32
nerve growth facto	A26431	μ.	425	8.1	102.5	31
laminin alpha 5 ch	T10053	ผ	3635	8.1	103.5	30

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A;Map position: 12p13-12p13
A;Introns: 46/1; 90/1; 150/1; 180/1; 220/1
C;Superfamily: CD27 antigen; Receptor repeat homology
C;Superfamily: CD27 antigen; Plycoprotein; homodimer; phosphoprotein; receptor; surface
E;1-20/Domain: signal sequence #status predicted <SIG>
F;1-20/Domain: signal sequence #status predicted <MAT>
F;21-260/Product: CD27 antigen #status predicted <EXT>
F;21-21/Domain: NGF receptor repeat homology <NG1>
F;27-63/Domain: NGF receptor repeat homology <NG2>
F;121-188/Region: proline/serine/threonine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
A46517
CD27 antigen precursor - human
CD27 antigen precursor - human
N;Alternate names: CD27L receptor; T cell activation antigen CD27
N;Alternate names (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Comment: A soluble CD27 found in serum and urine is formed by proteolysis. C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M63928; NID:g180084; PIDN:AAA58411.1; PID:g180085
A;Note: sequence extracted from NCBI backbone (NCBIN:60285, NCBIP:60289)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-58, 'A', (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The T cell activation antigen CD27 is a member of the nerve growth factor/the A;Reference number: A46454; MUID:92013149
A;Accession: A46454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: sequence extracted from NCBI backbone (NCBIP:120386)
A;Note: authors propose an alternative repeat pattern
R;Camerini, D.; Walz, G.; Loenen, W.A.; Borst, J.; Seed, B.
J. Immunol, 147, 3165-3169, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Loenen, W.A.; Gravestein, L.A.; Beumer, S.; Mellef, C.J.; Hagemeljer, A.; Borst, J. Immunol. 149, 3937-3943, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 18-Jun-1993 #sequence_revision 22-Apr-1995 #text_change 22-Jun-1999
C;Accession: A46517; A46454
C;Accession: A46517; A46454
C;Accession: A46517; A46454
                                                                                                                                                                                                                                                      F;192-211/Domain: transmembrane #status predicted <TMN>
F;212-260/Domain: intracellular #status predicted <INT>
F;95/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                            F; 192-211/Domain: F; 212-260/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: CD27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Genomic organization and chromosomal localization of the human CD27 gene. A; Reference number: A46517; MUID:93094588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:132582; OMIM:186711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-260 <LOE>
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                                                                                                                                                             Query Match
Best Local :
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                                                          CQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHH---KCQ 59
CPERHYWAQGKLC--CQMCEPGTFLVKDCDQ-HRKTAQCDPCIP-GVSFSPDHHTRPHCE 82
                                                                                                                              l Similarity
72; Conserv
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25.9%;
                                                                                                                           29;
                                                                                                                           Score 152.5; DB 1;
Pred. No. 1.6e-05;
9; Mismatches 78;
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                                                                                                                                                                                        Length 260;
                                                                                                                                  99;
                                                                                                                           Gaps
                                                                                                                                  18;
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A;Molecule type: protein
A;Residues: 30-38;41-53, X',55-79,'XX',82-94,'NK';'XX',100-104;107-128;162-167,'X',169-A;Residues: 30-38;41-53, X',55-79,'XX',82-94,'NK';'XX',100-104;107-128;162-167,'X',169-A;Note: the purified protein, called tumor necrosis factor binding protein, is a solubl R;Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of rA;Reference number: A38281; MUID:91017509
A;Accession: A38281; MUID:91017509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession of the type: mRNA
A; Molecule type: mRNA
A; Residues: 1-455 <SCH>
A; Cross-references: GB:M33294; NID:g339744; F
A; Cross-references: Maurer-Fogy, I; Kroenke, M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-De
C:Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057;
R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A:Title: Structure of the human TNF receptor 1 (p60) gene (TNRF1) and A:Reference number: A38208; MUID:92250049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M58286; GB:M33480;
A;Experimental source: placenta
A;Note: part of this sequence, including
R;Schall, T.J.; Lewis, M.; Koller, K.J.;
Cell 61, 361-370, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M75864; GB:M75865; R;Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Cell 61, 351-359, 1990
                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-455 <HIM>
A; Cross-references: GB:M63121;
A; Accession: C36555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A36555;
A; Accession: A36555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell 61, 361-370, 1990
A;Title: Molecular cloning
A;Reference number: A34900;
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A; Residues: 1-455 <LOE>
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A; Molecule type: DNA
A; Residues: 1-455 <FUC>
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         R;Nophar,
                                       A; Note: the
                                                                  A; Cross-references: GB:M37764
                                                                                          A; Residues:
                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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DNA Cell Biol.
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N;Contains: tumor necrosis factor
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   Y.; Kemper, O.; Brakebusch,
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                                                                                       1-455 <GRA>
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9, 705-715, 1990
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      codon ch, c.;
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Lee, A.; R
   TGG for res
Engelmann,
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Gentz, R.;
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      residue
ann, H.;
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371 as
Zwang,
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Pfizenmaier,
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      Aderka,
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D.; Holtmann
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atanaga, T.
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      F;168-196/Domain:
F;212-234/Domain:
                                                         F;127-167/Domain:
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A; Residues: 1-13 <KEM>
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A; Residues: 1-455 < NOP>
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A;Cross-references: GDB:125913; OMIM:191190
A;Cross-references: GDB:125913; OMIM:191190
A;Map position: 12913.2-12p13.2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/C;Superfamily; tumor necrosis factor receptor type 1; NGF receptor receptor; cromain: signal sequence #status predicted <SIG>F;1-21/Domain: signal sequence #status predicted <SIG>F;2-455/Product: tumor necrosis factor receptor 1 #status predicted F;30-211/Domain: extracellular #status predicted <EXT>F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha protein 1)
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A; Residues: 41-43; 'X', 45-53, 'V', 55-57, 'XK', 60
A; Experimental source: renal failure patient u
R; Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A; Title: Two tumor necrosis factor binding pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: JT0758; MUID:94085779
A;Accession: JT0758
A;Molecula ---
                    F:44-82/Domain: NGF receptor repeat homology <NG1>F:84-126/Domain: NGF receptor repeat homology <NG2>
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A;Residues: 41-43,'X',45-53,'X',55-57 <SEC>
A;Residues: 41-43,'X',45-53,'X',55-57 <SEC>
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, Eur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purificat A;Reference number: A60231; MUID:90292116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X55313;
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tle: Soluble forms of tumor necrosis factor
  NGF receptor repeat
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1, including its
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amino and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human
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predicted

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N;Alternate names: tumor necrosis factor receptor, 55K
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #text_change 01-Dec-2000
C;Date: 30-Jun-1992 #text_change 01-Dec-2000
C;Accession: A38634; B40254; S16677; S19021; I54532; I57826
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necro
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                                                                                                                              R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Less
Immunogenetics 34, 338-340, 1991
A;Title: Molecular cloning and expression of
A;Reference number: S19021; MUID:92039815
                                                                                                                                                                                                                                                                                           A;Title: Cloning, expression and cross-linking analysis of the murine p55 A;Reference number: S16677; MUID:91285014
A;Accession: S16677
                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M60468; NID:g199825; R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, Eur. J. Immunol. 21, 1649-1656, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, Mol. Cell. Biol. 11, 3020-3026, 1914 A;Title: Molecular cloning and expression of the A;Reference number: A40254; MUID:91246168
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                                                                 A; Molecule type: mRNA
A; Residues: 1-454 < ROT>
                                                                                                                                                                                                                     A;Residues: 1-454 <BAR>
A;Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1;
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A; Residues: 1-454 <GO2>
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R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Cope
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A; Residues: 1-454 <LEW>
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                                       A;Cross-references: EMBL:X57796; NID:g54848;
                                                                                                         A; Accession: S19021
                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
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66; Conservative
                                                                                                                                                                                             Brockhaus,
450-451, 1994
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21.3%;
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                                                                                                                                                                                                  R.; Lesslauer,
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A.P.; Kissonerghis,
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                                          PIDN:CAA40936.1;
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                                                                                                                                                     receptor type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type 2 murine
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is, A.M.; Gray,
                                          PID: 954849
                                                                                                                                                                                                                       PID:g53579
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A;Cross-references: GB:L26349; NID:g430732; PIDN:AAA59361.1; R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Stei Mol. Immunol. 30, 165-176, 1993
A;Title: Genomic organization and promoter function of the mu A;Reference number: I57826; MUID:93156721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-212/Domain: extracellular #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393,'G',395-454 <RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M76656; C;Comment: This protein is one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: I54532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma A; Reference number: I54532; MUID:94245292
RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                    163
                                                                        335 APTSVQ 340
                                                                                                                      222 IPQQQQ 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 KTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIPCKETQ
                                                                                                                                                                                                                                                                                                                                                                                                                        97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 CPQGKYVHSKNNSICCTKCHKGTYLVSDCP-SPGRDTVCRECEKGTFTASQNYLRQCLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
                                                                                                                                                                                                                                                                                                                   VVFTLAFLGLFF--LYCK----
                                                                                                                                                                                                                                                                    ILLGLCLLSFIFISLMCRYPRWRPEVYSIICR--DPVPVKEEKAGKPLTPAPSPAFSPTS
                                                                                                                                                                                                                                                                                                                                                                      NTVCNCHAGFFLRESECVPCSHCKKNEE----CMKLCLPPPLANVTNPQDSG-TAVLLPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITC-AVINRVQKVNCTATSNAVCG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGH-HKCQSC
                                                                                                                                                                     GFNPTLGFSTPGFSSPVSSTP--ISPIFGPSNWHFMPPVSEVVPTQGADPLLYESLCSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-454 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                -GG--LQDQECIPCTKQTPTSEVQCAFQLSLVEADAPTVPPQEATLVALVSSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                   -ESQVSWAPGSLAQLF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.4%;
21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 145; DB 1;
Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                     -QFFNRHCQRGGLLQFEADKTAKEESLFPVPPSKETS
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                                                                                                                                                                                                                      -SLDSVP 221
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CD27 antigen precursor - mouse
N;Alternate names: CD27L receptor; T cell activation antigen
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 22-Apr-1995 #text_char

R:Gravestein, L.A.; Blom, B.; Nolten, L.A. Eur. J. Immunol. 23, 943-950, 1993 A;Title: Cloning and expression of murine A;Reference number: A49053; MUID:93209296

Nolten,

L.A.;

Vries,

(F)

van der

Horst, G.; Ossendor

#text_change 11-Sep-1998

CD27: de

comparison with 4-1BB,

another lympho

C; Accession: A49053

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A;Accession: A49053
A;Molecule type: mmNA
A;Residues: 1-250 GCRA>
A;Note: sequence extracted from NCBI backbone (NCBIN:128168, NCBIP:128169)
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: duplication; 9lycoprotein; homodimer; receptor; surface antigen;
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-20/Domain: signal sequence #status predicted <MAT>
F;21-250/Product: CD27 antigen #status predicted <EXT>
F;27-63/Domain: NGF receptor repeat homology <NG1>
F;65-105/Domain: NGF receptor repeat homology <NG2>
F:65-105/Domain: NGF receptor repeat homology <NG2>
F:65-105/Domain: NGF receptor repeat homology <NG2>
                                                                                                              F;44-194/Domain: extracellular cysteine rich #status predicted F;44-82/Domain: NGF receptor repeat homology <NG1>F;84-126/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                                                  C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor F;1-29/Domain: signal sequence #status predicted <SIG> F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Suter, B.; Pauli, U. Gene 163, 263-266, 1995
A;Title: Cloning of the cDNA encoding the A;Reference number: JC4302; MUID:96011645
A;Accession: JC4302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor necrosis factor receptor p55 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      망
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                                                  F;54,145,151/Binding site:
                                                                                                                                                                                                                                                               A; Gene: tnfr
C; Superfamily:
                                                                                                                                                                                                                                                                                                             A; Experimental source: kidney C; Genetics:
                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 1-7 <SU2>
                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: A; Accession: PC4093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;183-202/Domain: transmembrane *status predicted <TMN> F;203-250/Domain: intracellular *status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;121-179/Region: proline/serine/threonine-rich
                                                                     211-231/Domain: transmembrane #status predicted <TMM>
         Query
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 LAFLGLFFLYCKQFFNRHCQRGGLLQFEADKTAKEESLFP--VPPSKETSAESQVSWAPG
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         Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPDKHYWTGGGLC--CRMCEPGTFFVKDCEQDRTA-AQCDPCIPGTSFSPDYHTRPHCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLAQLESLDSVPIPQQQQGPE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMFL-IFVLGAILFFHQRRNHGP----NEDRQAVPEEPCPYSCPREEEGSA---
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                                                                                                                                                                                                                                                        tumor necrosis factor receptor type 1; NGF receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                            GB:U19994;
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25.7%;
                                                     carbohydrate
       . 6%;
                                                                                                                                                                                                                                                                                                                                   cell line
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Pred. No. 8.
       Score
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    134.5;
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ches 97;
                                             (covalent) #status predicted
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Length 461;
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A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of A;Reference number: I54182; MUID:93252381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Accession: I54182
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I54182
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A; Residues: 1-435 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor necrosis factor receptor 2-related protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                      222
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                                                                                                                                                                                                                                   163
                                                                            266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 QDTICNCHSGFFLRDKECVSCVNCKNADCKNLCPATSETRNDFQDTGTTVLLPLVIFFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 CPQGKYSHPQNRSICCTKCHKGTYLHNDC-LGPGLDTDCRECDNGTFTASENHLTQCLSC 102
                                                                                                                                                                                                                                                                                                                                                                                                                              4
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                                                                                                              PSKETSAESQVSWAPGSLAQLF --
                                                                                                                                                  SGTMLM - - - LAVLLPLAFFLLLATVFSCIWKSHPSLCRKLG
                                                                                                                                                                                       ATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRH----CQRGGLLQFEADKTAKEESLFPVP 193
                                                                                                                                                                                                                             GNNHCVPCKAGHFQNTSSPSARCQPHTRCENQ-GLVEAAPGTAQSDTTCKNPLEPLPPEM 221
                                                                                                                                                                                                                                                                   QDQECIPC-----TKQTPTSEVQ----CAFQLSLVEADAPT-----------VPPQE 136
                                                                                                                                                                                                                                                                                                         PCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGK 162
                                                                                                                                                                                                                                                                                                                                                  TCAVINRVQKV-NCTATSNAVC
                                                                                                                                                                                                                                                                                                                                                                                      QEKEYYEPQHR-ICCSRCPPGTYVSAKC--SRIRDTVCATCAENSYNEHWNYLTICQLCR 102
                                                                                                                                                                                                                                                                                                                                                                                                                          QENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHK-CQSCI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary;
                                                                          PQGEGPNPVAGSWEPPKAHPYFPDLVQPLLPISGDVSPVSTGLPAAPVLEAGVPQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKCRSEMSQVEISPCTVDRDTVCG-CRKNQYRKYWSETLFQCLNCSLCPNGTVQLPCLEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTESPVPSFSPISSPTFTPCDWSNIKVTSPPKEIAPPPQGAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSAESQV-SWAPGSLAQLFSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLAFFLFVGLACRYQRWKPKLYSIICGKSTPVKEGEPEPLATAPSFGPITTFSPIPSFSP 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A-----FLGLFFLYCK---QFFNRHCQRG-GLLQFEADKTAKEES-----LFPVPPSKE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITC-AVINRVQKVNCTATSNAVCGDCLPRFYRK----TRIGGLQDQEC-----IPCTKQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGH-HKCQSC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:L04270; NID:g339761; PIDN:AAA36757.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 134; DB 2;
Pred. No. 0.0009;
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0; Mismatches 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109; Indels
                                                                                                              --SLDSVP----IPQQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -EATLVALVSSLLVVFTL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human
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                                                                                                                                                    -SLLKRR
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seq

tumor necrosis

factor receptor

2 precursor [validated]

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A;Molecule type: mRNA
A;Residues: 1-195, 'R,'197-461 <KOH>
A;Residues: 1-195, 'R,'197-461 <KOH>
A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
Cytokine 2, 231-237, 1990
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A;Reference number: A48416; MUID:91370690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A;Note: sequence extracted from NCBI backbone (NCBIN:63368; NCBIP:63371)
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and A;Reference number: A36007; MUID:90349572
A;Accession: A36007
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kuhnert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the A;Reference number: 138094; MUID:95121934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence A;Reference number: A35010; MUID:90110215
A;Accession: B35010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 116-140, 'P',142-195, 'R',197-362, 'T',364-461 <HEL>
A; Cross-references: GB:M35857; NID:9339751; PIDN:AAA63262.1; PID:9339752
R; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2 (;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000 C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094 R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.: Science 248, 1019-1023, 1990 A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and A;Reference number: A35356; MUID:90260639
                                                                                                                  A; Map position: 1p36.2-1p36
                                                                                                                                                                                                                                                                                                               A; Molecule type:
A; Residues: 1-37
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: I38094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 27-31 <ENG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 23-40;65-69;136-141;300-306 <LOE>
R; Engelmann, H.; Novick, D.; Wallach, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 265, 20131-20138, 1990
A;Title: Purification and partial amino acid sequence analysis of two distinct tumor A;Reference number: A23666; MUID:91056048
A;Accession: A23666
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                                                                                                                                                                                                                                                                           A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated
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A;Accession: A36475
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   ;Note: the list of introns is incomplete;Superfamily: tumor necrosis factor rece
                                                                                                                                                     Cross-references: GDB:125914; OMIM:191191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
                                                                                                                                                                                                    GDB: TNFR2
                                       list of introns is
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                                                                                                                                                                                                                                                                                                                   <RES>
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                                                                                                                                                                                                                                                               EMBL: X80021; NID: g666044; PIDN: CAA56324.1; PID: g825701
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   receptor
type 2;
NGF receptor repeat homology
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RESULT
GQRTT1
F;127-167/Domain: NGF receptor repeat homology <NG3>F;168-204/Domain: NGF receptor repeat homology <NG4>F;168-204/Domain: transmembrane #status predicted <NEM>F;235-461/Domain: intracellular #status predicted <INT>F;54,151,201/Binding site: carbohydrate (Asn) (covalent
                                                                                                                             F;30-211/Domain: extracellular #status predicted <EXT>
F;30-201/Product: tumor necrosis factor binding protein #status
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
                                                                                                                                                                                                                                                                                                            A;Residues: 1-461 <HIM>
A;Residues: 1-461 <HIM>
A;Cross-references: GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachecting) C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor necrosis factor receptor 1 precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30 Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22 Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Molecular cloning and expression of human and A;Reference number: A36555; MUID:91090841 A;Accession: B36555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Himmler, A.; Maurer-Fogy, I.;
DNA Cell Biol. 9, 705-715, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;262-279/Domain:
F;280-461/Domain:
F;171,193/Binding
                                                                                                                                                                                                                                    F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted
                                                                                                                                                                                                                                                                C; Keywords: duplication; glycoprotein; receptor; trans F;1-29/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: B36555
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F;78-119/Domain: NGF receptor repeat homology <NG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: duplication; glycoprotein; receptor; transmembrane protein F;1-22/Domain: signal sequence *status predicted <SIG> F;23-416/Product: tumor necrosis factor receptor 2 *status experimenta
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 KETSAESQVSWAPGSLAQLFSLD-SVPIPQQQQGP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSSLESSAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLIIGVVNCVIMTQVKKKPLCLQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPS-PPAEGSTGDFALPVGLIVGVTA--LG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LODQECIPCTKQT--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITCAVINRVQKVNCTATSNAVCGDCLPRFY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRLREYYDQTAQ-MCCSKCSPGQHAKVFC--TKTSDTVCDSCEDSTYTQLWNWVPECLSC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSRCSSDQVETQACTREQNRIC-TCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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intracellular #status predicted <INT>
site: carbohydrate (Asn) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ALDRRAPTRNQPQAP 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kroenke, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
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                                                                                                                                                                                                                                                                                            transmembrane
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                                                                                                                                                                                  predicted
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                                                                                                                                                                                                                                                                                                                                                (cachectin)
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                                                                                                                                                                                                                                       <MAT>
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;54,151,201/Binding site:

carbohydrate (Asn) (covalent) #status

predicted

Query Match

Local

. Similarity 53; Conserv

Conservative

16;

10.2%; 25.7%;

Score 130; DB 1 Pred. No. 0.002;

DB 1;

Length 461;

Indels

48;

Gaps

10;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
B32393
T-cell antigen 4-1BB precursor - mouse
T-cell antigen 4-1BB precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C;Accession: B32393; 14879
C;Accession: B3233; 14879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; R;Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T. J. Immunol. 152, 2256-2262, 1994
A;Title: Genomic Organization and Chromosomal Localization of A;Reference number: I48879; MUID:94179805
A;Accession: I48879
A;Status: Preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rioc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989 A;Title: CDNA sequence of two inducible T-cell genes A;Reference number: A32393; MUID:89184547 A:Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-256 < RES>
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A; Residues: 1-256 < KWO>
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Best Local
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            233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                              QVSWAPGSLAQLFSLDSVPIPQQQQG 228
                                                                                                                            VSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQFEADKTAKEESLFPVPPSKETSAES
                                                                                                                                                                 RPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLAL
                                                                                                                                                                                           IPCTK-------QTPTSE--VQC-----AFQLSLVEADAPTVPP-----QEATL-VAL 142
                                                                                                                                                                                                                                           F-CSSTHNAEC-ECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCSLGTFNDQNGTGVC
                                                                                                                                                                                                                                                                                           VNCTATSNAVCGDCLPRFY-----
                                                                                                                                                                                                                                                                                                                             VGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPNCNICRVCAGYFRFKK
                                                                                                                                                                                                                                                                                                                                                                 VTCQRCGPGQELSKDCGYGEGGDAY---CTACPPRRYKSSWGHHKCQSCITCAVINRVQK 72
                                                                                        TSALLL -- ALIFITLLFSVLKWI ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1 CD27 antigen; NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4-1BB protein #status predicted <MAT>
          AQEEDACSCRCPQEEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                10.2%; Score 129.5; DB 24.8%; Pred. No. 0.0013;
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        249
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                                                                                      -RKKFPHIFKQPFKKTTGA-- 232
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Вр
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R;Cascino, I.; Flucci, G.; Papoff, G.; Ruberti, J. Immunol. 154, 2706-2713, 1995
A;Title: Three functional soluble forms of the A;Reference number: 137383; MUID:95181785
A;Accession: 137383
                                                                                                                                                                                                                                                                                                                                                                                                                        FAS soluble protein - human C;Species: Homo sapiens (man) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-314 < RES>
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C;Keywords: transmembrane protein
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>
                                                                                                                                                                                        A;Cross-references: EMBL:Z47993; NID:g728578; PIDN:CAA88031.1;
                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDB.
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Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A;Title: Aberrant transcription caused by the insertion of
A;Reference number: A47254; MUID:93189576
A;Accession: A47254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptosis-mediating membrane-associated polypeptide Fas - mouse C; Species: Mus musculus (house mouse)
C; Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change C; Accession: A46484; A47254
R; Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.;
J. Immunol. 148, 1274-1279, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: MRL lpr/lpr
A; Note: sequence extracted from NCBI backbone (NCBIN:126850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: nucleic acid
A; Residues: 1-96 < ADA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226
A;Experimental source: BAM3 macrophage cell line
A;Experimental source: BAM3 macrophage cell line
A;Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)
B:Adachi M: Bitton Communication NCBI backbone (NCBIN:81544, NCBIP:81545)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-327 <WAT>
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CHKPCPPGERKARDCTV-NGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEI 117
                                         CQR-CGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGH--HKCQSCITCAVINRVQ-KV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCITCAVINRVQ-KVNCTATSNAVCGDCLPRFY-----RKTRIGGLQDQECIPCTKQT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCSEGLY---QGGPFCCQPCQPGKKKVEDCKM-NGGTPTCAPCTEGKEYMDKNHYADKCR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHH--KCQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTSEVQCAFQLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RCTLCDEEHGLEVETNCTLTQNTKC-KCKPDFYCDSPGCEHCVRCASCEHGTLEPC---T 154
                                                                                                    40;
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46; Conserv
                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                        Fiucci, G.; Papoff, G.; Ruberti, 4, 2706-2713, 1995
                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                   10.1%;
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25.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                             Score 129; DB 2;
Pred. No. 0.0018;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 129.5;
Pred. No. 0.0
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                                                                                                                                         Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --PLVFIY-RKYRKRKC
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A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human new A;Reference number: JT0752; MUID:94085794

A;Recession: JT0752

A;Molecule type: mRNA

A;Residues: 1-106,'R',108-255 <SCH>
C;Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necrosic comment: This protein recomposizes soluble, cell-surface bound or extracellular matrix C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>
F:138-213/Domain: transmembrane #status predicted <TMM>
F:138-213/Domain: transmembrane #status predicted <TMM>
F:138-213/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted F:234,235/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
kinase-defective Eph-family receptor protein precursor - human C;Species: Homo sapiens (man) C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 24-Sep-1999 C;Accession: JC5526 C;Accession: JC5526 R;Matsuoka, H.; Iwata, N.; Ito, M.; Shimoyama, M.; Nagata, A.; Chihara, K.; Biochem. Biophys. Res. Commun. 235, 487-492, 1997 A;Title: Expression of a kinase-defective Eph-like receptor in the normal human control of the second con
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Gene 134, 295-298, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 SLDGKSVLVNGTKERDVVCGPSPADLSPGASSVTPPAPAREPGHSPQIISFFLALTSTAL
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        Eph-like receptor in the normal human brain.
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                                                                                      Nagata, A.; Chihara, K.; Takai,
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                                     81-124/Domain: NGF receptor repeat homology <NG4>
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C:Keywords: transmembrane protein
F:1-21/Domain: signal sequence #status predicted <
F:22-324/Product: Fas antigen #status predicted <M
F:22-324/Product: Fas antigen #status predicted <M
F:44-79/Domain: NGF receptor repeat homology <NG4:
F:171-188/Domain: transmembrane #status predicted
                                                                                                                                        A; Introns:
C; Superfami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: JC2395; PC2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1-16/Domain: signal sequence #status predicted <SIG>F;3-53-456/Domain: fibronectin type III repeat homology <FN3B>F;472-556/Domain: fibronectin type III repeat homology <FN3B>F;578-603/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-1006 <MAT>
A;Cross-references: DDB:D83492; NID:g2281007; PIDN:BAA21560.1; PID:d1022410; PID:g2:
C;Comment: This protein is highly homologous to Eph-family receptor tyrosine kinase,
                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                               A; Experimental source: liver
                                                                                                                                                                                                                                     A; Cross-references: DDBJ:D26113;
                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-62, 'RFT' <KI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 198, 666-6
A; Title: A variant mRNA species encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Kimura, K.; Wakatsuki, T.; Yamamot
Biochem. Biophys. Res. Commun. 198,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;663-907/Domain: protein kinase homology <KIN>F;661-669/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: hep
                                                                                                                                                                                                                                                                                                           A; Accession:
                                                                                                                                                                                                                                                                                                                               A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: DDBJ:D26112;
                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-324 <KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: JC2395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fas antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 7q33-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
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A;Accession: JC5526
A;Status: nucleic acid sequence not shown
                                                                                                                                        Superfamily: NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 QWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQSCITCAVINRV
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ommun. 198, 666-674,
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25.7%;
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                                                                                                                                                                                                                                     NID: 9468488;
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7; Mismatches
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                                                                                                                                                                                                                                  PIDN:BAA05109.1;
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rat

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59 CHKPCPPGERKARDCTV-NGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEI 117
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Search completed: October 26, 2002, 21:10:13 Job time : 21 secs

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